



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 06:39 PM UTC

PDB ID : 1YHK / pdb_00001yhk
Title : Trypanosoma cruzi farnesyl diphosphate synthase
Authors : Gabelli, S.B.; McLellan, J.S.; Montalvetti, A.; Oldfield, E.; Docampo, R.; Amzel, L.M.
Deposited on : 2005-01-09
Resolution : 2.10 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

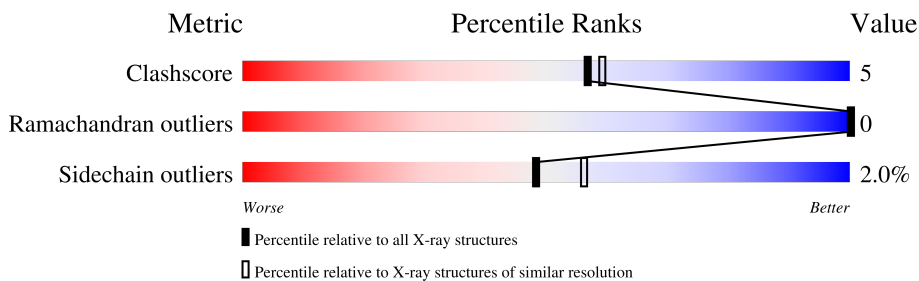
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.10 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
Clashscore	190562	7164 (2.10-2.10)
Ramachandran outliers	187476	7099 (2.10-2.10)
Sidechain outliers	187428	7100 (2.10-2.10)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	362	 80% 17% ..

2 Entry composition [i](#)

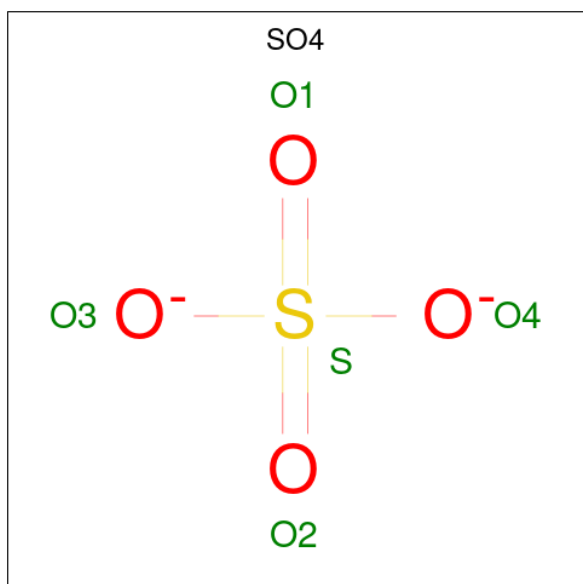
There are 3 unique types of molecules in this entry. The entry contains 3163 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called farnesyl pyrophosphate synthase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	360	Total	C	N	O	S	0	0	0
			2873	1845	469	536	23			

- Molecule 2 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	O	S	0	0
			5	4	1		
2	A	1	Total	O	S	0	0
			5	4	1		

- Molecule 3 is water.

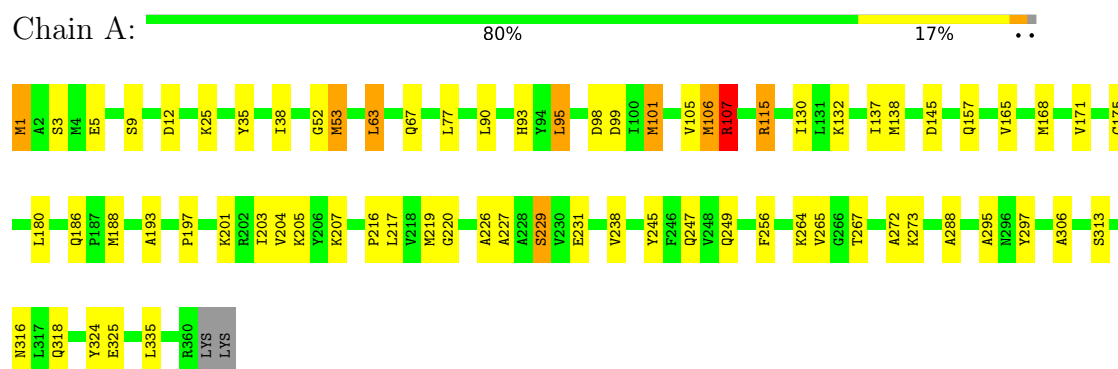
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	280	Total	O	0	0
			280	280		

3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

Note EDS was not executed.

- Molecule 1: farnesyl pyrophosphate synthase



4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	P 61 2 2	Depositor
Cell constants a, b, c, α , β , γ	57.92Å 57.92Å 397.70Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	65.94 – 2.10	Depositor
% Data completeness (in resolution range)	94.0 (65.94-2.10)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	REFMAC 5.1.24	Depositor
R, R_{free}	0.173 , 0.227	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	3163	wwPDB-VP
Average B, all atoms (Å ²)	31.0	wwPDB-VP

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: SO4

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	1.70	32/2938 (1.1%)	1.33	13/3982 (0.3%)

All (32) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	168	MET	SD-CE	-12.25	1.49	1.79
1	A	101	MET	SD-CE	-9.43	1.55	1.79
1	A	106	MET	SD-CE	9.02	2.02	1.79
1	A	105	VAL	CA-CB	8.52	1.64	1.55
1	A	186	GLN	CG-CD	7.20	1.70	1.52
1	A	231	GLU	CD-OE1	7.17	1.39	1.25
1	A	220	GLY	CA-C	7.14	1.60	1.52
1	A	188	MET	SD-CE	6.69	1.96	1.79
1	A	288	ALA	CA-CB	6.53	1.63	1.53
1	A	295	ALA	CA-CB	6.41	1.64	1.53
1	A	52	GLY	C-O	-6.28	1.16	1.23
1	A	217	LEU	C-O	-6.06	1.17	1.24
1	A	165	VAL	CA-CB	-5.94	1.47	1.54
1	A	38	ILE	C-O	5.91	1.31	1.24
1	A	335	LEU	C-O	-5.56	1.17	1.24
1	A	157	GLN	CB-CG	-5.54	1.35	1.52
1	A	168	MET	C-O	5.44	1.30	1.24
1	A	53	MET	SD-CE	5.39	1.93	1.79
1	A	264	LYS	CD-CE	5.35	1.68	1.52
1	A	1	MET	CG-SD	5.25	1.93	1.80
1	A	306	ALA	CA-CB	5.24	1.61	1.53
1	A	171	VAL	N-CA	-5.21	1.40	1.46
1	A	324	TYR	C-O	-5.21	1.18	1.24
1	A	227	ALA	CA-CB	-5.18	1.45	1.53
1	A	316	ASN	CA-C	5.18	1.59	1.53
1	A	264	LYS	CE-NZ	5.14	1.64	1.49

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	313	SER	C-O	-5.09	1.18	1.24
1	A	217	LEU	CA-C	5.06	1.59	1.52
1	A	171	VAL	C-O	-5.02	1.17	1.24
1	A	216	PRO	CA-C	5.02	1.59	1.52
1	A	95	LEU	N-CA	-5.01	1.40	1.46
1	A	107	ARG	NE-CZ	-5.00	1.27	1.33

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	205	LYS	N-CA-C	-6.03	104.62	111.07
1	A	229	SER	N-CA-C	5.98	120.19	113.01
1	A	90	LEU	N-CA-C	-5.85	104.99	111.36
1	A	130	ILE	N-CA-C	-5.77	104.71	111.00
1	A	138	MET	CB-CA-C	-5.61	101.84	110.81
1	A	12	ASP	N-CA-C	-5.30	105.50	111.28
1	A	107	ARG	CG-CD-NE	-5.27	100.40	112.00
1	A	9	SER	CA-C-O	5.27	126.03	119.97
1	A	193	ALA	N-CA-C	5.26	117.70	111.33
1	A	137	ILE	N-CA-C	-5.24	105.28	110.62
1	A	63	LEU	N-CA-C	-5.23	105.76	111.82
1	A	256	PHE	N-CA-C	5.22	119.92	113.50
1	A	219	MET	CG-SD-CE	5.14	112.21	100.90

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2873	0	2830	26	0
2	A	10	0	0	0	0
3	A	280	0	0	9	1
All	All	3163	0	2830	26	1

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including

hydrogen atoms). The all-atom clashscore for this structure is 5.

All (26) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:106:MET:CE	1:A:106:MET:SD	2.02	1.46
1:A:175:CYS:HB3	3:A:618:HOH:O	1.51	1.07
1:A:145:ASP:HB3	3:A:643:HOH:O	1.79	0.83
1:A:180:LEU:HD22	3:A:579:HOH:O	1.81	0.80
1:A:106:MET:CE	1:A:106:MET:CG	2.69	0.71
1:A:204:VAL:HG22	1:A:247:GLN:HG2	1.79	0.64
1:A:249:GLN:OE1	3:A:649:HOH:O	2.18	0.55
1:A:226:ALA:O	1:A:229:SER:HB3	2.07	0.54
1:A:203:ILE:HG13	3:A:622:HOH:O	2.07	0.54
1:A:197:PRO:O	1:A:201:LYS:HG3	2.08	0.53
1:A:203:ILE:O	1:A:207:LYS:HB3	2.08	0.52
1:A:67:GLN:HB3	3:A:632:HOH:O	2.11	0.51
1:A:93:HIS:NE2	1:A:132:LYS:HE3	2.27	0.49
1:A:25:LYS:HE2	3:A:633:HOH:O	2.12	0.49
1:A:115:ARG:NH2	3:A:464:HOH:O	2.35	0.48
1:A:93:HIS:CD2	1:A:132:LYS:HE3	2.49	0.48
1:A:1:MET:HG3	1:A:3:SER:HB2	1.96	0.47
1:A:318:GLN:CG	3:A:628:HOH:O	2.62	0.47
1:A:35:TYR:C	1:A:35:TYR:CD1	2.92	0.46
1:A:63:LEU:HD11	1:A:77:LEU:HG	1.99	0.43
1:A:99:ASP:OD2	1:A:107:ARG:HD2	2.18	0.43
1:A:98:ASP:HA	1:A:101:MET:HE3	2.00	0.43
1:A:3:SER:HB3	1:A:53:MET:HE1	2.01	0.43
1:A:272:ALA:HA	1:A:297:TYR:CE2	2.54	0.42
1:A:265:VAL:HG13	1:A:267:THR:HG23	2.02	0.42
1:A:245:TYR:CE2	1:A:325:GLU:HG3	2.55	0.41

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:495:HOH:O	3:A:647:HOH:O[1_655]	2.11	0.09

5.3 Torsion angles

5.3.1 Protein backbone

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	358/362 (99%)	350 (98%)	8 (2%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	307/309 (99%)	301 (98%)	6 (2%)	48	56

All (6) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	5	GLU
1	A	95	LEU
1	A	107	ARG
1	A	115	ARG
1	A	238	VAL
1	A	273	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	21	GLN
1	A	91	GLN

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Mol	Chain	Res	Type
1	A	157	GLN
1	A	186	GLN
1	A	316	ASN
1	A	318	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

2 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
2	SO4	A	371	-	4,4,4	0.76	0	6,6,6	0.41	0
2	SO4	A	370	-	4,4,4	0.48	0	6,6,6	0.95	0

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

EDS was not executed - this section is therefore empty.

6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates ⓘ

EDS was not executed - this section is therefore empty.

6.4 Ligands ⓘ

EDS was not executed - this section is therefore empty.

6.5 Other polymers ⓘ

EDS was not executed - this section is therefore empty.